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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/966,561

DATE: 01/14/2002
 TIME: 10:29:11

Input Set : N:\Crf3\RULE60\09966561.raw
 Output Set: N:\CRF3\01142002\I966561.raw

1 <110> APPLICANT: University of Southern California
 2 Miller, Carol A.
 3 Dong, Zhao Hui
 4 Zhang, Yan
 5 <120> TITLE OF INVENTION: APOPTOSIS INHIBITION
 6 <130> FILE REFERENCE: 13761-724
 7 <140> CURRENT APPLICATION NUMBER: US/09/966,561
 8 <141> CURRENT FILING DATE: 2001-09-27
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/419,694
 W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-14
 11 <160> NUMBER OF SEQ ID NOS: 3
 12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2836
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (1)...(2136)
 21 <400> SEQUENCE: 1
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 23 Met Ala Glu Arg Glu Ser Gly Gly Leu Gly Gly Ala Ala Ser Pro
 24 1 5 10 15
 25 ccc gcc gcc tcc ccg ttc ctg ggg ctg cac atc gct tcg cct ccc aat 96
 26 Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser Pro Pro Asn
 27 20 25 30
 28 ttc agg ctc acc cat gac atc agc ctg gag gag ttt gag gat gaa gac 144
 29 Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu Asp Glu Asp
 30 35 40 45
 31 ctc tcg gag atc act gat gag tgt ggc atc agc tta cag tgc aaa gac 192
 32 Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln Cys Lys Asp
 33 50 55 60
 34 acc ctg tcc tta cgg ccc ccg cgc ggc ggg ctg ctc tct gcg ggc ggc 240
 35 Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser Ala Gly Gly
 36 65 70 75 80
 37 ggc ggc gcg ggg agc cgg ttg cag gcc gag atg ctg cag atg gac ctg 288
 38 Gly Gly Ala Gly Ser Arg Leu Gln Ala Glu Met Leu Gln Met Asp Leu
 39 85 90 95
 40 atc gac gcg acg ggg gac act ccc ggg gcc gag gac gac gag gag gac 336
 41 Ile Asp Ala Thr Gly Asp Thr Pro Gly Ala Glu Asp Asp Glu Glu Asp
 42 100 105 110
 43 gac gac gag gag cgc gcg gcc cgg cgg gga gcg ggg ccc aag 384
 44 Asp Asp Glu Glu Arg Ala Ala Arg Arg Pro Gly Ala Gly Pro Pro Lys
 45 115 120 125
 46 gcc gaa tcc ggc cag gag ccg gcg tcc cgc ggc cag ggc cag agc caa 432
 47 Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Gly Gln Gly Gln Ser Gln
 48 130 135 140

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49	ggc cag agc cag ggc ccg ggc agc ggg gac acg tac cgg ccc aag cgg	480
50	Gly Gln Ser Gln Gly Pro Gly Ser Gly Asp Thr Tyr Arg Pro Lys Arg	
51	145 150 155 160	
52	ccc acc acg ctc aac ctc ttt ccg cag gtg ccg cgg tct cag gac aca	528
53	Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr	
54	165 170 175	
55	ctg aat aat aat tct ctg ggc aaa aag cac agt tgg cag gat cgg gtg	576
56	Leu Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg Val	
57	180 185 190	
58	tct cga tca tcc tca ccc ctg aag aca ggg gag cag aca cca ccg cat	624
59	Ser Arg Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His	
60	195 200 205	
61	gaa cac atc tgc ctg agc gag ctg ccc ccc cag agc ggc ccc gcc	672
62	Glu His Ile Cys Leu Ser Glu Glu Leu Pro Pro Gln Ser Gly Pro Ala	
63	210 215 220	
64	ccc acc aca gat cga ggc acc tcc acc gac agc cct tgc cgc cgc agc	720
65	Pro Thr Thr Asp Arg Gly Thr Ser Thr Asp Ser Pro Cys Arg Arg Ser	
66	225 230 235 240	
67	aca gcc acc cag atg gca cct ccg ggt ggt ccc cct gct gcc ccg cct	768
68	Thr Ala Thr Gln Met Ala Pro Pro Gly Gly Pro Pro Ala Ala Pro Pro	
69	245 250 255	
70	ggg ggt cgg ggc cac tcg cat cga gac cga atc cac tac cag gcc gat	816
71	Gly Gly Arg Gly His Ser His Arg Asp Arg Ile His Tyr Gln Ala Asp	
72	260 265 270	
73	gtg cga cta gag gcc act gag gag atc tac ctg acc cca gtg cag agg	864
74	Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg	
75	275 280 285	
76	ccc cca gac gct gca gag ccc acc tcc gcc ttc ctg ccg ccc act gag	912
77	Pro Pro Asp Ala Ala Glu Pro Thr Ser Ala Phe Leu Pro Pro Thr Glu	
78	290 295 300	
79	agc cgg atg tca gtc agc tcc gat cca gac cct gcc gcc tac ccc tcc	960
80	Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Pro Ser	
81	305 310 315 320	
82	acg gca ggg cgg ccg cac ccc tcc atc agt gaa gag gaa gag ggc ttc	1008
83	Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Glu Gly Phe	
84	325 330 335	
85	gac tgc ctg tcg tcc cca gag cgg gct gag ccc cca ggc gga ggg tgg	1056
86	Asp Cys Leu Ser Ser Pro Glu Arg Ala Glu Pro Pro Gly Gly Trp	
87	340 345 350	
88	cgg ggg agc ctg ggg gag ccg cca cct cca cgg gcc tct ctg agc	1104
89	Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Arg Ala Ser Leu Ser	
90	355 360 365	
91	tcg gac acc agc gcc ctg tcc tat gac tct gtc aag tac acg ctg gtg	1152
92	Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val	
93	370 375 380	
94	gta gat gag cat gca cag ctg gag gtg agc ctg cgg ccg tgc ttc	1200
95	Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe	
96	385 390 395 400	
97	gga gac tac agt gac gag agt gac tct gcc acc gtc tat gac aac tgt	1248

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Input Set : N:\Crf3\RULE60\09966561.raw
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98	Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys		
99	405	410	415
100	gcc tcc gtc tcc tcg ccc tat gag tcg gcc atc gga gag gaa tat gag	1296	
101	Ala Ser Val Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu		
102	420	425	430
103	gag gcc ccg cgg ccc cag ccc cct gcc tgc ctc tcc gag gac tcc acg	1344	
104	Glu Ala Pro Arg Pro Gln Pro Pro Ala Cys Leu Ser Glu Asp Ser Thr		
105	435	440	445
106	cct gat gaa ccc gac gtc cat ttc tcc aag aaa ttc ctg aac gtc ttc	1392	
107	Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe		
108	450	455	460
109	atg agt ggc cgc tcc cgc tcc agt gct gag tcc ttc ggg ctg ttc	1440	
110	Met Ser Gly Arg Ser Arg Ser Ser Ala Glu Ser Phe Gly Leu Phe		
111	465	470	475
112	tcc tgc atc atc aac ggg gag gag cag gag cag acc cac ccc gcc ata	1488	
113	Ser Cys Ile Ile Asn Gly Glu Glu Gln Gln Thr His Arg Ala Ile		
114	485	490	495
115	ttc agg ttt gtg cct cga cac gaa gac gaa ctt gag ctg gaa gtg gat	1536	
116	Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Val Asp		
117	500	505	510
118	gac cct ctg cta gtg gag ctc cag gct gaa gac tac tgg tac gag gcc	1584	
119	Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala		
120	515	520	525
121	tac aac atg cgc act ggt gcc cgg ggt gtc ttt cct gcc tat tac gcc	1632	
122	Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala		
123	530	535	540
124	atc gag gtc acc aag gag ccc gag cac atg gca gcc ctg gcc aaa aac	1680	
125	Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn		
126	545	550	555
127	560		
128	agt gac tgg gtg gac cag ttc cgg gtg aag ttc ctg ggc tca gtc cag	1728	
129	Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln		
130	565	570	575
131	gtt ccc tat cac aag ggc aat gac gtc ctc tgt gct gct atg caa aag	1776	
132	Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala Ala Met Gln Lys		
133	580	585	590
134	att gcc acc acc cgc cgg ctc acc gtg cac ttt aac ccg ccc tcc agc	1824	
135	Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn Pro Pro Ser Ser		
136	595	600	605
137	tgt gtc ctg gag atc agc gtg cgg ggt gtg aag ata ggc gtc aag gcc	1872	
138	Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile Gly Val Lys Ala		
139	610	615	620
140	gat gac tcc cag gag gcc aag ggg aat aaa tgt agc cac ttt ttc cag	1920	
141	Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser His Phe Phe Gln		
142	625	630	635
143	640		
144	tta aaa aac atc tct ttc tgc gga tat cat cca aag aac aac aag tac	1968	
145	Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys Asn Asn Lys Tyr		
146	645	650	655
	ttt ggg ttc atc acc aag cac ccc gcc gac cac cgg ttt gcc tgc cac	2016	
	Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg Phe Ala Cys His		

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147	660	665	670	
148	gtc ttt gtg tct gaa gac tcc acc aaa gcc ctg gca gag tcc gtg ggg			2064
149	Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala Glu Ser Val Gly			
150	675	680	685	
151	aga gca ttc cag cag ttc tac aag cag ttt gtg gag tac acc tgc ccc			2112
152	Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu Tyr Thr Cys Pro			
153	690	695	700	
154	aca gaa gat atc tac ctg gag tag ctgtgcagcc ccgcctctg cgtccccag			2166
155	Thr Glu Asp Ile Tyr Leu Glu			
156	705	710		
157	ccctcaggcc agtgcagga cagctggctg ctgacaggat gtggcactgc ttgaggaggg			2226
158	gcacctgcga ccgcccagg acaaggaagt gggggccgct gcggcagggt aggggagggt			2286
159	ggggcaatgg ggagaggcaa atgcagttta ttgtaatata tgggattaga ttcatctatg			2346
160	gagggcagag tgggctgcct ggggattggg agggcacagg cttggggagc aggtctctgg			2406
161	cagagaagga tgtccgttcc aggagcacac gcgcctgcgc catcctgggc cttacctccc			2466
162	ctgcccaggcc tcggcgctg tggctctgc cttgatgaag cccgtgtcct gccttgatga			2526
163	agcctgtgcc acctgcaagt gcccgcctg cccctgccc acccccgaaag accctgagct			2586
164	caggctgagc ccagccaccc ccaaggact ttccagtagg aatggcaac aggtgaagtc			2646
165	cctgttctca gtcggcgtcat ctggggtegg gggctctgc cactgacctc accggcatgc			2706
166	tggcctgtgg caggcctagg acctcaggcg gggaggagga gcgcgcagccc gtccgaaaag			2766
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172	<212> TYPE: PRT			
173	<213> ORGANISM: Homo sapiens			
174	<400> SEQUENCE: 2			
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177	Pro Ala Ala Ser Pro Phe Leu Gly Leu His Ile Ala Ser Pro Pro Asn			
178	20	25	30	
179	Phe Arg Leu Thr His Asp Ile Ser Leu Glu Glu Phe Glu Asp Glu Asp			
180	35	40	45	
181	Leu Ser Glu Ile Thr Asp Glu Cys Gly Ile Ser Leu Gln Cys Lys Asp			
182	50	55	60	
183	Thr Leu Ser Leu Arg Pro Pro Arg Ala Gly Leu Leu Ser Ala Gly Gly			
184	65	70	75	80
185	Gly Gly Ala Gly Ser Arg Leu Gln Ala Glu Met Leu Gln Met Asp Leu			
186	85	90	95	
187	Ile Asp Ala Thr Gly Asp Thr Pro Gly Ala Glu Asp Asp Glu Glu Asp			
188	100	105	110	
189	Asp Asp Glu Glu Arg Ala Ala Arg Arg Pro Gly Ala Gly Pro Pro Lys			
190	115	120	125	
191	Ala Glu Ser Gly Gln Glu Pro Ala Ser Arg Gly Gln Gly Gln Ser Gln			
192	130	135	140	
193	Gly Gln Ser Gln Gly Pro Gly Ser Gly Asp Thr Tyr Arg Pro Lys Arg			
194	145	150	155	160
195	Pro Thr Thr Leu Asn Leu Phe Pro Gln Val Pro Arg Ser Gln Asp Thr			
196	165	170	175	

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197 Leu Asn Asn Asn Ser Leu Gly Lys Lys His Ser Trp Gln Asp Arg Val
 198 180 185 190
 199 Ser Arg Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His
 200 195 200 205
 201 Glu His Ile Cys Leu Ser Glu Glu Leu Pro Pro Gln Ser Gly Pro Ala
 202 210 215 220
 203 Pro Thr Thr Asp Arg Gly Thr Ser Thr Asp Ser Pro Cys Arg Arg Ser
 204 225 230 235 240
 205 Thr Ala Thr Gln Met Ala Pro Pro Gly Gly Pro Pro Ala Ala Pro Pro
 206 245 250 255
 207 Gly Gly Arg Gly His Ser His Arg Asp Arg Ile His Tyr Gln Ala Asp
 208 260 265 270
 209 Val Arg Leu Glu Ala Thr Glu Glu Ile Tyr Leu Thr Pro Val Gln Arg
 210 275 280 285
 211 Pro Pro Asp Ala Ala Glu Pro Thr Ser Ala Phe Leu Pro Pro Thr Glu
 212 290 295 300
 213 Ser Arg Met Ser Val Ser Ser Asp Pro Asp Pro Ala Ala Tyr Pro Ser
 214 305 310 315 320
 215 Thr Ala Gly Arg Pro His Pro Ser Ile Ser Glu Glu Glu Gly Phe
 216 325 330 335
 217 Asp Cys Leu Ser Ser Pro Glu Arg Ala Glu Pro Pro Gly Gly Gly Trp
 218 340 345 350
 219 Arg Gly Ser Leu Gly Glu Pro Pro Pro Pro Arg Ala Ser Leu Ser
 220 355 360 365
 221 Ser Asp Thr Ser Ala Leu Ser Tyr Asp Ser Val Lys Tyr Thr Leu Val
 222 370 375 380
 223 Val Asp Glu His Ala Gln Leu Glu Leu Val Ser Leu Arg Pro Cys Phe
 224 385 390 395 400
 225 Gly Asp Tyr Ser Asp Glu Ser Asp Ser Ala Thr Val Tyr Asp Asn Cys
 226 405 410 415
 227 Ala Ser Val Ser Ser Pro Tyr Glu Ser Ala Ile Gly Glu Glu Tyr Glu
 228 420 425 430
 229 Glu Ala Pro Arg Pro Gln Pro Pro Ala Cys Leu Ser Glu Asp Ser Thr
 230 435 440 445
 231 Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe Leu Asn Val Phe
 232 450 455 460
 233 Met Ser Gly Arg Ser Arg Ser Ser Ala Glu Ser Phe Gly Leu Phe
 234 465 470 475 480
 235 Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr His Arg Ala Ile
 236 485 490 495
 237 Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu Leu Glu Val Asp
 238 500 505 510
 239 Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr Trp Tyr Glu Ala
 240 515 520 525
 241 Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro Ala Tyr Tyr Ala
 242 530 535 540
 243 Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala Leu Ala Lys Asn
 244 545 550 555 560
 245 Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu Gly Ser Val Gln

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09966561.raw
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